CPP 1: Active Matter I (joint session BP/CPP/DY)

Time: Monday 9:30–12:45 Location: BAR/SCHÖ

CPP 1.1 Mon 9:30 BAR/SCHÖ

Bayesian inference of magnetosensing in a magnetotactic bacterium — •Sascha Lambert[1], Emilie Gachon[2], Damien Faivre[2], and Stefan Klumpp[1] — [1]University of Göttingen, Institute for the Dynamics of Complex Systems, Friedrich-Hund-Platz 1, 37077 Göttingen, Germany. — [2]Aix Marseille Université, CEA, CNRS, BIAM, 13115 Saint-Paul-Lez-Durance, France.

Magnetotactic bacteria are often assumed to align only passively with external magnetic fields, yet recent observations of the magnetotactic bacterium SS-5 reveal a pronounced increase in swimming speed under geomagnetic conditions. Because flagellated microorganisms typically follow helical paths, magnetic torques could, in principle, straighten their trajectories and create an apparent increase in speed, offering a purely mechanical explanation. We test this hypothesis using a physical swimming model based on Active Brownian Particles that incorporates magnetic torques, rotational propulsion, and helical motion, and we explore the relevant parameter space using Bayesian inference constrained by three-dimensional trajectory data. Posterior predictive simulations demonstrate that the mechanically induced increase in apparent speed is far too small to account for the experimental observations, even under extreme parameter choices. The results quantitatively rule out swaying as a sufficient explanation for the behaviour of SS-5 and instead support the presence of an active magnetic sensing mechanism.

CPP 1.2 Mon 9:45 BAR/SCHÖ

Vorticity-induced surfing and trapping in porous media — •Pallabi Das[1], Mirko Residori[1], Axel Voigt[2,3,4], Suvendu Mandal[5], and Christina Kurzthaler[1,3,4] — [1]Max Planck Institute for the Physics of Complex Systems, Germany — [2]Institute of Scientific Computing, TU Dresden, Germany — [3]Center for Systems Biology Dresden, Germany — [4]Cluster of Excellence, Physics of Life, TU Dresden, Germany — [5]TU Darmstadt, Germany

Microorganisms often encounter strong confinement and complex hydrodynamic flows while navigating their habitats. Combining finite-element methods and stochastic simulations, we study the interplay of active transport and heterogeneous flows in dense porous channels. We find that swimming always slows down the traversal of agents across the channel, giving rise to robust power-law tails of their exit-time distributions. These exit-time distributions collapse onto a universal master curve with a scaling exponent of $\approx 3/2$ across a wide range of packing fractions and motility parameters, which can be rationalized by a scaling relation. We further identify a new motility pattern where agents alternate between *trapping* along fast streams and extended *surfing* phases, the latter determining the power-law exponent. Unexpectedly, trapping occurs in the flow backbone itself – not only at obstacle boundaries – due to vorticity-induced reorientation in the highly-heterogeneous flow environment. These findings provide a fundamentally new active transport mechanism with direct implications for biofilm clogging and the design of novel microrobots capable of operating in heterogeneous media.

CPP 1.3 Mon 10:00 BAR/SCHÖ

Adhesion Patterns in Gliding Filamentous Cyanobacteria — •Elias Fischer[1], Paul Nieschwitz[2], Stefan Karpitschka[2], and Holger Stark[1] — [1]Institute of Physics and Astronomy, TU Berlin, Germany — [2]Department of Physics, Universität Konstanz, Germany

Filamentous cyanobacteria play an important role in many ecosystems and the carbon cycle of our planet. They exhibit gliding motility when in contact with solid surfaces or each other. Despite their ecological relevance and increased use in biotech applications, the exact nature of the force-generating process remains not fully understood.

Our recent measurements of filamentous cyanobacteria gliding across flat surfaces and visualized in kymographs show spatio-temporal adhesion regions along the filament, indicating an intrinsic helical shape. Based on our a novel approach for modeling the mechanical aspects of individual cyanobacteria filaments, we are able to interpret the complex kymograph patterns. Each filament is modeled as a helical chain of thin cylindrical segments in 3D with bending and twisting elasticity. The filaments interact with nearby surfaces and filaments via a hard-core repulsion and an exponentially decaying adhesion force. Importantly, the propulsion forces that push the filament forward are only applied locally at surface-contacting segments.

Our simulated kymographs reveal how both the helical shape and the adhesion strength strongly influence the filament's gliding speed and the dynamics of the surface-attachment regions. Thereby, we crucially contribute to the understanding of how real filamentous cyanobacteria generate their propulsion forces.

CPP 1.4 Mon 10:15 BAR/SCHÖ

The 3D chirality of malaria parasites determines their motion patterns in 2D and originates at the apical pole — •Leon Lettermann[1], Mirko Singer[2], Smilla Steinbrück[2,3], Falko Ziebert[1], Sachie Kanatani[3], Photini Sinnis[3], Friedrich Frischknecht[2], and Ulrich Schwarz[1] — [1]Institute for Theoretical Physics & BioQuant, Heidelberg University — [2]Parasitology, Center for Infectious Diseases, Heidelberg University — [3]School of Public Health and Malaria Research Institute, Johns Hopkins University

Plasmodium sporozoites, the slender forms of the malaria parasite injected by mosquitoes into the skins of their vertebrate hosts, provide a medically highly relevant model system for active chiral particles. Using 3D tracking in synthetic hydrogels, we show that sporozoites consistently move on right-handed helical trajectories. When they encounter a two-dimensional substrate, they switch to clockwise circular motion, whereas circling on glass in medium occurs with the opposite sense of rotation, suggesting on glass they try to invade the medium above. Using a sandwich assay, we demonstrate that chirality also determines the reverse transition from two-dimensional to three-dimensional motion. Combining these measurements with a theory for gliding motility allows us to identify the likely origin of chirality, namely an asymmetric distribution of adhesins. After confirming this via two-sided traction force microscopy, we finally use STED super-resolution microscopy to reveal a corresponding tilt in the apical ring complex. In summary, our analysis thus uncovers both the biological relevance and the molecular basis of chirality in the movement of malaria parasites.

CPP 1.5 Mon 10:30 BAR/SCHÖ

Squirmer dynamics in porous environments — •Mirko Residori[1], Christina Kurzthaler[1], and Sebastian Aland[2] — [1]Max Planck Institute for the Physics of Complex Systems — [2]TU Freiberg

We introduce a computational framework for simulating the dynamics of micro-swimmers in complex porous environments. Specifically, we adopt a diffusive domain approach to represent the surface of a micro-swimmer, modeled as a squirmer. This method ensures accurate and stable finite-element simulations, even in highly confined geometries. Validation against analytical and numerical benchmarks confirms the model*s accuracy and robustness. We then apply it to explore squirmer motion in heterogeneous porous media, revealing how hydrodynamic interactions lead to behaviors such as dynamic trapping due to hydrodynamically induced re-orientations. Moreover, we demonstrate that the squirmer parameter and the repulsive potential critically influence a squirmer's ability to navigate and escape confinement. The proposed framework offers a versatile and efficient tool for studying active motion in complex fluids and provides new insights into micro-swimmer transport and control in natural and engineered systems.

CPP 1.6 Mon 10:45 BAR/SCHÖ

Dynamics of passive tracers in active dumbbell suspension — •Chandranshu Tiwari and Sunil P. Singh — Department of Physics, Indian Institute of Science Education and Research, Bhopal 462066, India.

The transport of passive tracers in active fluids exhibits rich dynamics arising from persistent interactions between active agents and the tracer. In our work, we employ Brownian dynamics simulations to investigate the dynamical behaviour of both isotropic(circular) and anisotropic(elliptical) tracers in active dumbbell suspension, considering only steric interactions. For circular tracers, we find that the speed shows a crossover from monotonically decreasing to increasing with tracer size as the dumbbells' speed is increased. The tracer's effective diffusion also displays a non-monotonic dependence on area fraction: the diffusivity first increases and then decreases at higher area fractions.

For anisotropic tracers, the characteristic non-monotonic trend persists. Moreover, their motion along the major and minor axes differs significantly. Anisotropic accumulation of active particles around the tracer generates direction-dependent forces and fluctuations, favouring motion along the major axis. Consequently, both the speed and diffusivity along the major axis exceed those along the minor axis.

15 min. break

Invited Talk CPP 1.7 Mon 11:15 BAR/SCHÖ

Modeling and inference of magnetotactic motility in complex environments — •Stefan Klumpp — Institute for the Dynamics of Complex Systems, University of Göttingen, Göttingen, Germany

Magnetotactic bacteria orient themselves and swim along field lines of the geomagnetic field. Their magnetically directed self-propelled motion makes them an instance of dipolar active matter. Here we focus on the interaction of these bacteria with walls or obstacles. Experiments in microfluidic systems show that interactions with walls result in (possibly transient) alignment parallel to the wall, which may compete with the alignment with the magnetic field. The dynamic behavior arising from the competition of the two alignments includes U-turn trajectories in circular chambers and trapping and escape dynamics in channels with overlapping cylindrical obstacles. In a phenomenological picture, the resulting motion can be described in an Active Brownian Particle model by introducing a wall torque that competes with the magnetic torque, which results in good agreement with experimental observations. Systematic Bayesian inference of the wall torque from observations shows that only a part of the torque function (dependence on incident angle) can be learned reliably from the data.

CPP 1.8 Mon 11:45 BAR/SCHÖ

Quantifying aggregation behaviour of filamentous cyanobacteria — •Elias Illing and Stefan Karpitschka — Fachbereich Physik, Universität Konstanz

Cyanobacteria are ubiquitous in nature, frequently causing ecological and economic harm by explosive growth, so called blooms.

We investigate the collective dynamics of entangled filamentous cyanobacteria in open liquid media, reminiscent of their aggregates found during later stages of blooms. We investigate the impact of illumination on the clustering and spreading of the bacteria and quantify the morphology of the bacterial aggregates by image analysis. We determine the critical density necessary for initial clustering and track the evolution of the subsequent stages, ranging from stable clusters to spreading mats. These states can be modulated by light intensity variations, potentially allowing for control of the morphological evolution of cyanobacterial aggregates.

CPP 1.9 Mon 12:00 BAR/SCHÖ

Dynamically Induced Spatial Segregation in Multi-Species Bacterial Bioconvection — •Mingqi Yan[1,2], Chenxi Wang[3], Oscar Gallardo-Navarro[4], Rinat Arbel-Goren[4], Joel Stavans[4], and Erwin Frey[1,2] — [1]Department of Physics, Ludwig-Maximilians-Universität München, Theresienstraße 37, 80333 München, Germany — [2]Max Planck School Matter to Life, Hofgartenstraße 8, 80539, München, Germany — [3]School of Science, Harbin Institute of Technology, 518055, Shenzhen, China — [4]Department of Physics of Complex Systems, Weizmann Institute of Science, 7610001, Rehovot, Israel

Bacterial bioconvection is a classic example of collective behavior in active matter, where upward-swimming bacteria create density instabilities leading to large-scale fluid flows. While this phenomenon is well-studied in single-species suspensions, natural environments are typically inhabited by diverse microbial communities. Here, we investigate the collective dynamics of multi-species bacterial suspensions. Combining experiments with a continuum model, we show that different bacterial species can spontaneously segregate into stable, spatially interlocked domains. Our theoretical analysis reveals that this segregation is not driven by biochemical antagonism but rather by the interplay between species-specific motility characteristics and the self-generated hydrodynamic flows. This work provides new insights into how physical interactions alone can drive the spatial organization of complex microbial communities.

CPP 1.10 Mon 12:15 BAR/SCHÖ

Light-switchable microbial rafts at air-liquid interfaces — •Gustav F. Nolte, Alexandros A. Fragkopoulos, Timo Völkl, Mechthild Rappold, and Oliver Bäumchen — University of Bayreuth, Experimental Physics V, 95447 Bayreuth, Germany

In biological active matter, clustering occurs across a wide range of time and length scales, from molecular assemblies such as actomyosin networks to macroscopic systems like fire ant rafts. Here, we report on a fast, light-switchable, and fully reversible clustering phenotype on the microscale, observed at air-liquid interfaces: the raft formation of the biciliated microalga *Chlamydomonas noctigama*.

C. noctigama is a relative of the model organism *Chlamydomonas reinhardtii*, which exhibits light-switchable adhesion and subsequent clustering at solid-liquid interfaces [1,2]. We show how the cluster morphology depends on cell density and discuss potential growth mechanisms by analyzing dynamics of individual clusters. Furthermore, we characterize the dependence of raft formation on the light spectrum and interfacial free energy. Using micropipette force spectroscopy [3], we show that single cells exploit capillary forces for light-switchable ciliary adhesion to the air-liquid interface, enabling raft formation. In their natural habitats, reversible clustering may provide an advantage by allowing cells to accumulate in locations optimal for photosynthesis while increasing resilience to environmental stress.

[1] C. T. Kreis, et al., *Nat. Phys.* **14**, 45 (2018).
[2] S. Till, et al., *Phy. Rev. Res.* **4**, L042046 (2022).
[3] M. Backholm and O. Bäumchen, *Nat. Protoc.* **14**, 594-615 (2019).

CPP 1.11 Mon 12:30 BAR/SCHÖ

Circadian gravitaxis: Photosynthetic microswimmers remodel local pH to actively tune vertical migration — Arkajyoti Ghoshal[1], Soumitree Mishra[1], Jayabrata Dhar[2], Hans-Peter Grossart[3,4], and •Anupam Sengupta[1,5] — [1]Physics of Living Matter, Department of Physics and Materials Science, University of Luxembourg, Luxembourg — [2]Department of Mechanical Engineering, National Institute of Technology Durgapur, India — [3]Department of Plankton and Microbial Ecology, Leibniz Institute of Freshwater Ecology and Inland Fisheries, Stechlin, Germany — [4]Institute of Biochemistry and Biology, Potsdam University, Germany — [5]Institute for Advanced Studies, University of Luxembourg, Luxembourg

Motile phytoplankton shuttle between bright surface waters and deeper nutrient rich layers, usually controlled by internal circadian clocks. Yet many species show irregular movements, defying the expected circadian rhythm. Studying a bloom forming photosynthetic species, we found that cells adjust their vertical migration by altering local pH, mediated by a shift in their gravitactic behavior. This self-modulation of pH generates sub-populations which are physiologically similar but swim differently, remaining vertically separated even under uniform conditions. Supported by a cell-level analysis and mathematical model, we confirm that the pH-mediated circadian shift is underpinned by morphological adjustments. Our results support a circadian gravitactic model in which diurnal pH control drives diversified migration, enhancing fitness particularly in acidifying oceans.